# Freeform Search

**Database:** US Pre-Grant Publication Full-Text Database
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EPO Abstracts Database
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Derwent World Patents Index
IBM Technical Disclosure Bulletins

**Term:** primer$1 ne

**Display:** 10 **Documents in Display Format:** - **Starting with Number** 1

**Generate:** ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search Clear Interrupt

## Search History

**DATE: Monday, October 30, 2006** **Purge Queries** Printable Copy Create Case

| Set Name side by side | Query | Hit Count | Set Name result set |
|---|---|---|---|
| *DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ* | | | |
| L4 | L3 and displace$4 | 28 | L4 |
| L3 | primer$1 near5 random near5 (constant or homologous) | 65 | L3 |
| *DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ* | | | |
| L2 | L1 and strand displace$4 | 7 | L2 |
| L1 | primer$1 near5 random near5 (constant or homologous) | 26 | L1 |

END OF SEARCH HISTORY

```
 s random (10a) primer#(10a)(constant sequence# or identical sequence#)
L1             0 RANDOM (10A) PRIMER#(10A)(CONSTANT SEQUENCE# OR IDENTICAL SEQUEN
                 CE#)

=> s (primer# or oligonucleotide#)(10a)random (10a)(constant or identical)
L2            32 (PRIMER# OR OLIGONUCLEOTIDE#)(10A) RANDOM (10A)(CONSTANT OR
                 IDENTICAL)

=> s l2 and (amplif######## or PCR or exten####)
L3            25 L2 AND (AMPLIF######## OR PCR OR EXTEN####)

=> s l3 and (strand (10a)displace####)
L4             0 L3 AND (STRAND (10A) DISPLACE####)

=> s l3 and displac####
L5             0 L3 AND DISPLAC####

=> dup rem l3
PROCESSING COMPLETED FOR L3
L6            13 DUP REM L3 (12 DUPLICATES REMOVED)

=> d l-13 bib ab kwic
'L-13' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files.  Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):end

=> d L6 1-13 bib ab kwic

L6   ANSWER 1 OF 13  CAPLUS  COPYRIGHT 2006 ACS on STN DUPLICATE 1
AN   2005:643920  CAPLUS
DN   144:267979
TI   Mutation of hepatitis B virus detected by hybridization in oligonucleotide
     array
AU   Lu, Yanqin; Han, Jinxiang; Huang, Haiyan; Zhu, Bo
CS   Key Laboratory for Bio-tech Drugs Ministry of Health, Shandong Medicinal
     Biotechnology Center, Jinan, 250062, Peop. Rep. China
SO   Zhonghua Weishengwuxue He Mianyixue Zazhi (2004), 24(4), 324-327
     CODEN: ZWMZDP; ISSN: 0254-5101
PB   Beijing Shengwu Zhipin Yanjiuso
DT   Journal
LA   Chinese
AB   12 Mutation sites located in S, pre-C, X and P region of hepatitis B virus
     genome were detected.  12 Pairs of oligonucleotide probes were designed in
     the antisense strand with amino linker and poly T15 spacer at their 5
     terminal, the length of which was 14-18bp.  Synthesized probes were
     immobilized on aldehyde modified glass slides.  One pair of PCR
     primers was used for amplification of the part of S, P region
     which contained 5 mutation sites and the other pair of primers for
     fragment of X and pre-C region which contained 7 mutation sites.  Both of
     upper primers were fluorescence labeled at their 5 terminal.
     Single-strand fluorescence marked DNA acquired by asym. PCR was
     hybridized to oligonucleotide array and signal intensities were collected
     after scanning.  Among 12 pos. serum samples, no mutation was detected in
     surface antigen.  While in pre-core and core region, T1752-A1764 mutant
     was observed in 2 specimens and A1896 mutant found in 3 specimens, 1 sample
     was tested to hold T1762-A1764 and A1896 simultaneously and no mutant was
     identified in other 6 samples.  Random DNA sequencing result was
     identical to the results of oligonucleotide array.
     Oligonucleotide array is a fast method to detect mutations in parallel.
AB   12 Mutation sites located in S, pre-C, X and P region of hepatitis B virus
     genome were detected.  12 Pairs of oligonucleotide probes were designed in
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IT DNA microarray technology
Hepatitis B virus
Mutation
PCR (polymerase chain reaction)
(oligonucleotide array detecting hepatitis B virus mutation)

L6 ANSWER 2 OF 13 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2
AN 2002:704114 CAPLUS
DN 138:86808
TI Identification of Taenia asiatica in China: molecular, morphological, and epidemiological analysis of a Luzhai isolate
AU Eom, Keeseon S.; Jeon, Hyung-Kyu; Kong, Yoon; Hwang, Ui Wook; Yang, Yichao; Li, Xueming; Xu, Longqi; Feng, Zheng; Pawlowski, Zbigniew S.; Rim, Han-Jong
CS Department of Parasitology and Medical Research Institute, Chungbuk National University College of Medicine, Chongju, Chungbuk, 360-763, S. Korea
SO Journal of Parasitology (2002), 88(4), 758-764
CODEN: JOPAA2; ISSN: 0022-3395
PB American Society of Parasitologists
DT Journal
LA English
AB Multiple anal. has characterized a recently described tapeworm of people, T. asiatica, in mainland China. Six adult tapeworms collected from people of the Zhuang minority residing in the southern part of China (Luzhai isolate) were comparatively analyzed with other tapeworms from people: T. asiatica (South Korea), T. saginata (Poland, Korea), and T. solium (People's Republic of China). Exptl. infections with eggs from the Luzhai isolate in pigs and cattle produced cysticerci, each with a hookletless scolex and with wartlike formations on the external surface of the bladder wall. There were rostellar protrusions in the scolices of adult worms. Random amplified polymorphic DNA anal. using 3 arbitrary primers produced bands identical to those of the Korean T. asiatica. Conversely, T. saginata and T. solium exhibited different banding patterns. Phylogenetic relationships inferred from the complete nucleotide sequences of the internal transcribed spacer 2 placed the Chinese tapeworms consistently within the T. asiatica clade by 96% bootstrapping value in the maximum likelihood anal., 96% in maximum parsimony, and 100% in neighbor joining. These collective data demonstrate that T. asiatica is sympatrically distributed with the other 2 species of Taenia in the human host in mainland China.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB Multiple anal. has characterized a recently described tapeworm of people, T. asiatica, in mainland China. Six adult tapeworms collected from people of the Zhuang minority residing in the southern part of China (Luzhai isolate) were comparatively analyzed with other tapeworms from people: T. asiatica (South Korea), T. saginata (Poland, Korea), and T. solium

(People's Republic of China). Exptl. infections with eggs from the Luzhai isolate in pigs and cattle produced cysticerci, each with a hookletless scolex and with wartlike formations on the external surface of the bladder wall. There were rostellar protrusions in the scolices of adult worms. Random amplified polymorphic DNA anal. using 3 arbitrary primers produced bands identical to those of the Korean T. asiatica. Conversely, T. saginata and T. solium exhibited different banding patterns. Phylogenetic relationships inferred from the complete nucleotide sequences of the internal transcribed spacer 2 placed the Chinese tapeworms consistently within the T. asiatica clade by 96% bootstrapping value in the maximum likelihood anal., 96% in maximum parsimony, and 100% in neighbor joining. These collective data demonstrate that T. asiatica is sympatrically distributed with the other 2 species of Taenia in the human host in mainland China.

L6 ANSWER 3 OF 13 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
AN 2001:127339 BIOSIS
DN PREV200100127339
TI Genetic diversity of Amblyseius longispinosus and A. womersleyi (Acari: Phytoseiidae) using RAPD analysis.
AU Yeh, Wen-Bin [Reprint author]; Ho, Chai-Lien; Hui, Cho-Fat; Ho, Chyi-Chen
CS Department of Biology, Kaohsing Medical University, 100 Shih-Chuan 1st Rd, Kaoshiung, 807, Taiwan
wbyeh@cc.kmu.edu.tw
SO Zhonghua Kunchong, (December, 2000) Vol. 20, No. 4, pp. 335-345. print.
ISSN: 0258-462X.
DT Article
LA Chinese
ED Entered STN: 14 Mar 2001
Last Updated on STN: 15 Feb 2002
AB Predatory mites of Amblyseius longispinosus and A. womersleyi are used to control spider mites. It has been considered that A. womerslei is a synonym of A. longispinosus since their identification character (dorsal setae L8) with intermediate length has been found. Random amplified polymorphic DNA (RAPD) was used to analysis the genetic diversity of these two morphologically similar mites. Genomic DNAs were extracted separately from egg, nymph, and adult either from A. longispinosus or A. womersleyi, respectively. The optimal reaction condition including the buffer and DNA template were determined. Sixty random primers were used to perform the amplification in a constant condition. The results of PCR amplification showed that the DNA template from egg, nymph, or adult of the same species gave a similar pattern. Whereas, the genetic similarity between A. longispinosus and A. womersleyi were very low either from rough (14.9%) or serious (8.3%) calculation. It implied that there was a great divergence between these 2 mites. Furthermore, the OPH-17 and OPH-18 primers were selected, they provided a clearly different pattern between A. longispinosus and A. womersleyi.
AB. . . is a synonym of A. longispinosus since their identification character (dorsal setae L8) with intermediate length has been found. Random amplified polymorphic DNA (RAPD) was used to analysis the genetic diversity of these two morphologically similar mites. Genomic DNAs were extracted. . .. from A. longispinosus or A. womersleyi, respectively. The optimal reaction condition including the buffer and DNA template were determined. Sixty random primers were used to perform the amplification in a constant condition. The results of PCR amplification showed that the DNA template from egg, nymph, or adult of the same species gave a similar pattern. Whereas, the. . .
IT Methods & Equipment
RAPD analysis [random amplified polymorphic DNA analysis]: molecular genetic method
IT Miscellaneous Descriptors
genetic method; identification characters; optimal reaction conditions

L6 ANSWER 4 OF 13 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
AN 2000:14364 BIOSIS
DN PREV200000014364
TI Highly specific recognition of primer RNA structures for 2'-OH priming reaction by bacterial reverse transcriptases.
AU Inouye, Sumiko; Hsu, Mei-Yin; Xu, Aiguo; Inouye, Masayori [Reprint author]
CS Dept. of Biochemistry, Robert Wood Johnson Medical School, 675 Hoes Lane, Piscataway, NJ, 08854, USA
SO Journal of Biological Chemistry, (Oct. 29, 1999) Vol. 274, No. 44, pp. 31236-31244. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 29 Dec 1999
Last Updated on STN: 31 Dec 2001
AB A minor population of Escherichia coli contains retro-elements called retrons, which encode reverse transcriptases (RT) to synthesize peculiar satellite DNAs called multicopy single-stranded DNA (msDNA). These RTs recognize specific RNA structures in their individual primer-template RNAs to initiate cDNA synthesis from the 2'-OH group of a specific internal G residue (branching G residue). The resulting products (msDNA) consist of RNA and single-stranded DNA, sharing hardly any sequence homology. Here, we investigated how RT-Ec86 recognizes the specific RNA structure in its primer-template RNA. On the basis of structural comparison with HIV-1 RT, domain exchanges were carried out between two E. coli RTs, RT-Ec86 and RT-Ec73. RT-Ec86 (320 residues) and RT-Ec73 (316 residues) share only 71 identical residues (22%). From the analysis of 10 such constructs, the C-terminal 91-residue sequence of RT-Ec86 was found to be essential for the recognition of the unique stem-loop structure and the branching G residue in the primer-template RNA for retron-Ec86. Using the SELEX (systematic evolution of ligands by exponential enrichment) method with RT-Ec86 and primer RNAs containing random sequences, the identical stem-loop structure (including the 3-U loop) to that found in the retron-Ec86 primer-template RNA was enriched. In addition, the highly conserved 4-base sequence (UAGC), including the branching G residue, was also enriched. These results indicate that the highly diverse C-terminal region recognizes specific stem-loop structures and the branching G residue located upstream of the stem-loop structure. The present results with seemingly primitive RNA-dependent DNA polymerases provide insight into the mechanisms for specific protein RNA recognition.
AB. . . in the primer-template RNA for retron-Ec86. Using the SELEX (systematic evolution of ligands by exponential enrichment) method with RT-Ec86 and primer RNAs containing random sequences, the identical stem-loop structure (including the 3-U loop) to that found in the retron-Ec86 primer-template RNA was enriched. In addition, the highly. . .
IT Methods & Equipment
PCR [polymerase chain reaction]: DNA amplification, amplification method, in-situ recombinant gene expression detection, sequencing techniques; affinity chromatography: liquid chromatography, purification method; binding assay: analytical method, binding assays;. . .

L6 ANSWER 5 OF 13 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
AN 2000:300179 BIOSIS
DN PREV200000300179
TI Regeneration of diploid intergeneric somatic hybrid plants between Microcitrus and Citrus via electrofusion.
AU Liu Ji-Hong [Reprint author]; Hu Chun-Gen [Reprint author]; Deng Xiu-Xin [Reprint author]
CS National Key Laboratory of Crop Genetic Improvements, Huazhong Agricultural University, Wuhan, 430070, China
SO Acta Botanica Sinica, (Nov., 1999) Vol. 41, No. 11, pp. 1177-1182. print.

CODEN: CHWHAY. ISSN: 0577-7496.
DT Article
LA Chinese
ED Entered STN: 12 Jul 2000
Last Updated on STN: 7 Jan 2002
AB Leaf-derived protoplasts of Rough lemon (Citrus jambhiri Lush, 2n = 2x = 18) were electrofused with embryogenic suspension protoplasts of its relative; Microcitrus papuana Swingle (2n = 2x = 18), with an intention of creating novel germplasm. Six plants were regenerated following protoplasts fusion. Cytological examination demonstrated that they were diploids with 18 chromosomes (2n = 2x = 18). RAPD (random amplified polymorphic DNA) analyses with six arbitrary 10-mer primers showed that the regenerated plants had identical band patterns to those of Rough lemon for primers OPA-07, OPAN-07, OPE-05 and OPA-08, whereas for the other two primers, OPA-04 and OPS-13, bands specific to M. papuana could be detected in the regenerated plants. Cytological and RAPD analysis revealed that the regenerated plants were diploid somatic hybrids between M. papuana and Rough lemon. The putative hybrids were morphologically similar to Rough lemon. This is the first report on production of diploid somatic hybrid plants between citrus with its related genus via symmetric fusion.
AB. . . regenerated following protoplasts fusion. Cytological examination demonstrated that they were diploids with 18 chromosomes (2n = 2x = 18). RAPD (random amplified polymorphic DNA) analyses with six arbitrary 10-mer primers showed that the regenerated plants had identical band patterns to those of Rough lemon for primers OPA-07, OPAN-07, OPE-05 and OPA-08, whereas for the other two primers,. . .

L6 ANSWER 6 OF 13 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3
AN 1999:373846 CAPLUS
DN 131:182227
TI Identification of Fusarium oxysporum f. sp. basilici isolated from soil, basil seed, and plants by RAPD analysis
AU Chiocchetti, Annalisa; Ghignone, Stefano; Minuto, Andrea; Gullino, M. Lodovica; Garibaldi, Angelo; Migheli, Quirico
CS Dipartimento di Protezione e Valorizzazione delle Risorse Agroforestali - Patologia vegetale, Universita di Torino, Grugliasco, I-10095, Italy
SO Plant Disease (1999), 83(6), 576-581
CODEN: PLDIDE; ISSN: 0191-2917
PB American Phytopathological Society
DT Journal
LA English
AB Fifty-two isolates of Fusarium oxysporum, obtained from infected basil plants, seed, flower residues, and soil from different growing areas in Italy and Israel, were analyzed by random amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR), coupled to a DNA extraction protocol from colonies grown on Fusarium-selective medium. In a pathogenicity assay, 35 isolates caused 32 to 92% disease on seedlings of the highly susceptible basil cultivar Fine verde, while 17 isolates were nonpathogenic on basil. Thirty of the F. oxysporum f. sp. basilici isolates obtained from soil or wilted plants gave identical amplification patterns using 31 different random primers. All tested primers allowed clear differentiation of F. oxysporum f. sp. basilici from representatives of other formae speciales and from nonpathogenic strains of F. oxysporum. RAPD profiles obtained from DNA of isolates extracted directly from cultures grown on Fusarium selective medium were identical to those obtained from DNA extracted from lyophilized mycelia.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB Fifty-two isolates of Fusarium oxysporum, obtained from infected basil plants, seed, flower residues, and soil from different growing areas in Italy and Israel, were analyzed by random amplified polymorphic

DNA-polymerase chain reaction (RAPD-PCR), coupled to a DNA extraction protocol from colonies grown on Fusarium-selective medium. In a pathogenicity assay, 35 isolates caused 32 to 92% disease on seedlings of the highly susceptible basil cultivar Fine verde, while 17 isolates were nonpathogenic on basil. Thirty of the F. oxysporum f. sp. basilici isolates obtained from soil or wilted plants gave identical amplification patterns using 31 different random primers. All tested primers allowed clear differentiation of F. oxysporum f. sp. basilici from representatives of other formae speciales and from nonpathogenic strains of F. oxysporum. RAPD profiles obtained from DNA of isolates extracted directly from cultures grown on Fusarium selective medium were identical to those obtained from DNA extracted from lyophilized mycelia.

L6 ANSWER 7 OF 13 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
AN 1999:300063 BIOSIS
DN PREV199900300063
TI PCR fragmentation of DNA.
AU Zheleznaya, L. A.; Kossykh, V. G.; Svad'bina, I. V.; Oshman, T. S.; Matvienko, N. I. [Reprint author]
CS Institute of Protein Research, Russian Academy of Sciences, Pushchino, Moscow Region, 142292, Russia
SO Biochemistry (Moscow), (April, 1999) Vol. 64, No. 4, pp. 447-453. print. CODEN: BIORAK. ISSN: 0006-2979.
DT Article
LA English
ED Entered STN: 12 Aug 1999
Last Updated on STN: 12 Aug 1999
AB A method has been developed to prepare random DNA fragments using PCR. First, two cycles are carried out at 16degreeC with the Klenow's fragment and oligonucleotides (random primers) with random 3'-sequences and the 5'-constant part containing the site for cloning with the site-specific endonuclease. The random primers can link to any DNA site, and random DNA fragments are formed during DNA synthesis. During the second cycle, after denaturation of the DNA and addition of the Klenow's fragment, the random primers can link to newly synthesized DNA strands, and after DNA synthesis single-stranded DNA fragments are produced which have a constant primer sequence at the 5'-end and a complementary to it sequence at the 3'-end. During the third cycle, the constant primer is added and double-stranded fragments with the constant primer sequences at both ends are formed during DNA synthesis. Incubation for 1 h at 37degreeC degrades the oligonucleotides used at the first stage due to endonuclease activity of the Klenow's fragment. Then routine PCR amplification is carried out using the constant primer. This method is more advantageous than hydrodynamic methods of DNA fragmentation widely used for "shotgun" cloning.
TI PCR fragmentation of DNA.
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IT Methods & Equipment
cloning: cloning method; PCR [polymerase chain reaction]: amplification method
IT Miscellaneous Descriptors
enzyme activity; DNA fragmentation

L6 ANSWER 8 OF 13 MEDLINE on STN
AN 1999250446 MEDLINE
DN PubMed ID: 10231588
TI PCR fragmentation of DNA.
AU Zheleznaya L A; Kossykh V G; Svad'bina I V; Oshman T S; Matvienko N I
CS Institute of Theoretical and Experimental Biophysics, Russian Academy of Sciences, Pushchino, Moscow Region, 142292, Russia.
SO Biochemistry. Biokhimii a, (1999 Apr) Vol. 64, No. 4, pp. 373-8. Journal code: 0376536. ISSN: 0006-2979.
CY RUSSIA: Russian Federation
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199907
ED Entered STN: 30 Jul 1999
Last Updated on STN: 30 Jul 1999
Entered Medline: 19 Jul 1999
AB A method has been developed to prepare random DNA fragments using PCR. First, two cycles are carried out at 16 degrees C with the Klenow's fragment and oligonucleotides (random primers) with random 3'-sequences and the 5'-constant part containing the site for cloning with the site-specific endonuclease. The random primers can link to any DNA site, and random DNA fragments are formed during DNA synthesis. During the second cycle, after denaturation of the DNA and addition of the Klenow's fragment, the random primers can link to newly synthesized DNA strands, and after DNA synthesis single-stranded DNA fragments are produced which have a constant primer sequence at the 5'-end and a complementary to it sequence at the 3'-end. During the third cycle, the constant primer is added and double-stranded fragments with the constant primer sequences at both ends are formed during DNA synthesis. Incubation for 1 h at 37 degrees C degrades the oligonucleotides used at the first stage due to endonuclease activity of the Klenow's fragment. Then routine PCR amplification is carried out using the constant primer. This method is more advantageous than hydrodynamic methods of DNA fragmentation widely used for "shotgun" cloning.
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L6 ANSWER 9 OF 13 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4
AN 1998:534160 CAPLUS
DN 129:273125
TI Phylogenetic analysis of dipterocarps using random amplified polymorphic DNA markers
AU Rath, Priyadarshini; Rajaseger, G.; Goh, Chong Jin; Kumar, Prakash P.
CS School of Biological Sciences, The National University of Singapore, Singapore, 119260, Singapore
SO Annals of Botany (London) (1998), 82(1), 61-65
CODEN: ANBOA4; ISSN: 0305-7364
PB Academic Press
DT Journal
LA English
AB The phylogenetic relationships among 12 species belonging to three

different genera (Shorea, Hopea and Anisoptera) of Dipterocarpaceae were studied using random amplified polymorphic DNA (RAPD) markers. A modified CTAB DNA extraction protocol was used to obtain tannin- and polysaccharide-free genomic DNA from mature leaves. Cluster anal. of data from six random primers placed the 12 species in three groups corresponding to their resp. genera. Four distinct nodes of Shorea spp. and two of Hopea spp. could be identified. Anisoptera megistocarpa served as an outgroup, and was unique when compared to the other genera examined RAPD profiles of five individuals of H. odorata with six random primers were identical, suggesting that there is little intraspecific variation in this species. The RAPD technique can thus be successfully applied for the study of phylogenetic relationships of this important group of tropical timber trees. (c) 1998 Annals of Botany Company.

RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Phylogenetic analysis of dipterocarps using random amplified polymorphic DNA markers

AB The phylogenetic relationships among 12 species belonging to three different genera (Shorea, Hopea and Anisoptera) of Dipterocarpaceae were studied using random amplified polymorphic DNA (RAPD) markers. A modified CTAB DNA extraction protocol was used to obtain tannin- and polysaccharide-free genomic DNA from mature leaves. Cluster anal. of data from six random primers placed the 12 species in three groups corresponding to their resp. genera. Four distinct nodes of Shorea spp. and two of Hopea spp. could be identified. Anisoptera megistocarpa served as an outgroup, and was unique when compared to the other genera examined RAPD profiles of five individuals of H. odorata with six random primers were identical, suggesting that there is little intraspecific variation in this species. The RAPD technique can thus be successfully applied for the study of phylogenetic relationships of this important group of tropical timber trees. (c) 1998 Annals of Botany Company.

L6 ANSWER 10 OF 13 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

AN 1997:272024 BIOSIS

DN PREV199799563742

TI Absence of DNA polymorphisms in Myzus persicae (Homoptera: Aphididae) in relation to their host plants.

AU Kim, H. J.; Boo, K. S.; Cho, K. H.

CS Dep. Agric. Biol., Coll. Agric. and Life Sci., Seoul Natl. Univ., Seoul, South Korea

SO Korean Journal of Applied Entomology, (1996) Vol. 35, No. 3, pp. 209-215. ISSN: 1225-0171.

DT Article

LA English

ED Entered STN: 24 Jun 1997
Last Updated on STN: 24 Jun 1997

AB DNA polymorphisms were analyzed for 8 clones of the green Peach aphid, Myzus persicae Sulzer, by random amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR). The insect has different host preferences and was even classified into two different species, M. persicae Sulzer and Myzus nicotinae Blackman by their morphological characters, but this point is still in argument. To identify the differences between two types of the green peach aphid by RAPD-PCR, the template DNA was extracted from 4 clones each of tobacco-feeding and non-tobacco-feeding forms and one hundred primers of 10-nucleotides-long were tested in PCR. The amplified DNAs were analyzed by agarose gel electrophoresis. Eighty-three primers gave amplified DNA fragments with 1 to 22 in number and 500 to 20,000 base pairs in length, but no amplification was observed in the other 17 primers. The average number of fragment per each amplification was about 13. In the case of 82 out of 83

random primers, band patterns of amplified DNA were identical among 8 clones, even though some differences were noticed in the intensity of specific bands. Polymorphism was detected by only one primer within the tobacco-feeding forms, but not between the two host types. The results did not detect any relationship between RAPD polymorphism and their host preference.

AB DNA polymorphisms were analyzed for 8 clones of the green Peach aphid, Myzus persicae Sulzer, by random amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR). The insect has different host preferences and was even classified into two different species, M. persicae Sulzer and Myzus nicotinae. . . but this point is still in argument. To identify the differences between two types of the green peach aphid by RAPD-PCR, the template DNA was extracted from 4 clones each of tobacco-feeding and non-tobacco-feeding forms and one hundred primers of 10-nucleotides-long were tested in PCR. The amplified DNAs were analyzed by agarose gel electrophoresis. Eighty-three primers gave amplified DNA fragments with 1 to 22 in number and 500 to 20,000 base pairs in length, but no amplification was observed in the other 17 primers. The average number of fragment per each amplification was about 13. In the case of 82 out of 83 random primers, band patterns of amplified DNA were identical among 8 clones, even though some differences were noticed in the intensity of specific bands. Polymorphism was detected by only. . .

IT Miscellaneous Descriptors
AGRICULTURAL PEST; DNA POLYMORPHISM; GENETIC METHOD; HOST; POPULATION GENETICS; RANDOM AMPLIFIED POLYMORPHIC DNA; TOBACCO-FEEDING FORM

L6 ANSWER 11 OF 13 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 5
AN 1996:384556 CAPLUS
DN 125:133818
TI Application of PCR-amplified DNA to differentiate the Ganoderma isolates
AU Hseu, Ruey-Shyang; Moncalvo, Jean-Marc; Wang, Huei-Fang; Wang, Hsi-Hua
CS Department Agricultural Chemistry, National Taiwan University, Taipei, Taiwan
SO Zhongguo Nongye Huaxue Huizhi (1996), 34(2), 129-143
CODEN: CKNHAA; ISSN: 0578-1736
PB Chinese Agricultural Chemical Society
DT Journal
LA English
AB Polysaccharides are rich in cell walls of the Ganoderma species. These compds. have been considered as a potential source of the immunomodulatory factor. These polysaccharides interfere with several mol. and genetic techniques. This presentation describes mol. biol. methods in detail using the polymerase chain reaction (PCR), which enables identification and understanding of the differentiation of Ganoderma isolates. First, a method is described to isolate DNA from both mycelia and basidiocarps which removes most of the polysaccharides which may interfere with the PCR reaction. Then, a procedure is described for PCR amplification and cycle-sequencing of the internal transcribed spacer (ITS) region of the ribosomal gene (rDNA), which differentiates between Ganoderma species. Strains of the G. tsugae complex sharing an identical ITS sequence can be differentiated by random amplified polymorphic DNA (RAPD-PCR ) produced with arbitrary primers. These procedures together with the oligonucleotide primers used in this work should also be appropriate for mol. identification of allied polypore fungi.
TI Application of PCR-amplified DNA to differentiate the Ganoderma isolates
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techniques. This presentation describes mol. biol. methods in detail using the polymerase chain reaction (PCR), which enables identification and understanding of the differentiation of Ganoderma isolates. First, a method is described to isolate DNA from both mycelia and basidiocarps which removes most of the polysaccharides which may interfere with the PCR reaction. Then, a procedure is described for PCR amplification and cycle-sequencing of the internal transcribed spacer (ITS) region of the ribosomal gene (rDNA), which differentiates between Ganoderma species. Strains of the G. tsugae complex sharing an identical ITS sequence can be differentiated by random amplified polymorphic DNA (RAPD-PCR ) produced with arbitrary primers. These procedures together with the oligonucleotide primers used in this work should also be appropriate for mol. identification of allied polypore fungi.

ST Ganoderma identification PCR rRNA gene sequence

IT Amauroderma rude
Fomitopsis rosea
Ganoderma
Ganoderma australe
Ganoderma gibbosum
Ganoderma lucidum
Ganoderma tsugae
Polymerase chain reaction
(application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(for rRNA; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT Deoxyribonucleic acids
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(preparation of; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT Ribonucleic acids, ribosomal
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(25 S, gene for; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(ITS1 (internal transcribed spacer 1), gene for; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(ITS2 (internal transcribed spacer 2), gene for; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT 179467-61-9
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer 4.8 SR; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT 179467-62-0
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer 5.8S; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT 179467-60-8
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer BMB-CR; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

IT 179467-64-2
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer LR 15; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 179467-63-1
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer LR 1; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 179467-65-3
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer LR 21; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 179467-66-4
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer LR 3; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 179467-67-5
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer LR 5; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 179467-68-6
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer LR 6; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 168461-87-8
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer LR 7; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 168461-86-7
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer LR OR; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 149721-30-2
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer R1; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 149721-31-3
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer R2; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 182028-64-4
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer R3; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 149721-28-8
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer R4; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 147304-84-5
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer R5; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 179467-58-4
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer SR 1R; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 179467-59-5
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR primer SR 6; application of PCR-amplified DNA to differentiate the Ganoderma isolates)
IT 154946-07-3, GenBank X78791 154946-23-3, GenBank X78792 154946-24-4, GenBank X78789 154981-81-4, GenBank X78753 154981-82-5, GenBank X78774 154981-85-8, GenBank X78754 154981-86-9, GenBank X78775 154981-87-0, GenBank X78780 154981-90-5, GenBank X78771 154981-96-1, GenBank X78741

154981-97-2, GenBank X78762 154981-98-3, GenBank X78743 154982-02-2, GenBank X78766 154982-03-3, GenBank X78776 154982-04-4, GenBank X78764 154982-16-8, GenBank X78747 154982-17-9, GenBank X78768 154982-20-4, GenBank X78778 154982-21-5, GenBank Z37097 154982-22-6, GenBank X78767 154982-23-7, GenBank X78748 154982-24-8, GenBank X78769 154982-33-9, GenBank X78750 157935-21-2, GenBank Z37021 157935-31-4, GenBank Z37073 157935-48-3, GenBank Z37026 157935-49-4, GenBank Z37053 157935-51-8, GenBank Z37077 157935-52-9, GenBank Z37027 157935-53-0, GenBank Z37029 157935-54-1, GenBank Z37030 157935-57-4, GenBank Z37055 157935-61-0, GenBank Z37078 157935-63-2, GenBank Z37080 160181-42-0, GenBank Z37096 160493-43-6, GenBank Z37094 166356-89-4, GenBank X87362 166356-99-6, GenBank X87352
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(nucleotide sequence; application of PCR-amplified DNA to differentiate the Ganoderma isolates)

L6 ANSWER 12 OF 13 MEDLINE on STN DUPLICATE 6
AN 95403942 MEDLINE
DN PubMed ID: 7673685
TI Investigation of a nosocomial outbreak of Pseudomonas aeruginosa pneumonia in an intensive care unit by random amplification of polymorphic DNA assay.
AU Kerr J R; Moore J E; Curran M D; Graham R; Webb C H; Lowry K G; Murphy P G; Wilson T S; Ferguson W P
CS Department of Bacteriology, Belfast City Hospital, Northern Ireland.
SO The Journal of hospital infection, (1995 Jun) Vol. 30, No. 2, pp. 125-31. Journal code: 8007166. ISSN: 0195-6701.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199510
ED Entered STN: 26 Oct 1995
Last Updated on STN: 26 Oct 1995
Entered Medline: 19 Oct 1995
AB From July to September 1993 in the intensive care unit of the Royal Victoria Hospital there were 10 cases of pneumonia associated with sputum culture of Pseudomonas aeruginosa. The isolates had an identical biotype and pyocine typing profile. The same strain of P. aeruginosa was recovered from the sink plug-hole in two rooms, and the tap handles and ventilator tubing in a third room. All strains were retrospectively typed by the random amplification of polymorphic DNA (RAPD) method using a 26-mer oligonucleotide primer, and were identical in profile. Recommendations to medical and nursing staff included secretion isolation precautions, terminal disinfection after patient discharge, use of disposable vinyl gloves by hospital staff for all body substance contacts, thorough handwashing with 4% chlorhexidine gluconate before and after dealing with all patient contacts, and prompt, appropriate antibiotic treatment for P. aeruginosa pneumonia. RAPD is a simple and effective method to determine the relatedness of P. aeruginosa isolates, and typing results are available within a single working day; thus dramatically increasing its clinical relevance over existing molecular methods.
TI Investigation of a nosocomial outbreak of Pseudomonas aeruginosa pneumonia in an intensive care unit by random amplification of polymorphic DNA assay.
AB . . . two rooms, and the tap handles and ventilator tubing in a third room. All strains were retrospectively typed by the random amplification of polymorphic DNA (RAPD) method using a 26-mer oligonucleotide primer, and were identical in profile. Recommendations to medical and nursing staff included secretion isolation precautions, terminal disinfection after patient discharge, use of disposable. . .

CT Bacterial Typing Techniques
*Cross Infection: EP, epidemiology
Cross Infection: MI, microbiology
*DNA, Bacterial: GE, genetics
*Gene Amplification
Humans
Infection Control: MT, methods
*Intensive Care Units
Northern Ireland: EP, epidemiology
*Pneumonia, Bacterial: EP, epidemiology
Pneumonia, Bacterial: MI,. . .

L6 ANSWER 13 OF 13 MEDLINE on STN DUPLICATE 7
AN 96108567 MEDLINE
DN PubMed ID: 8554698
TI Detection of T cell receptors in early rheumatoid arthritis synovial tissue.
AU Ramanujam T; Luchi M; Schumacher H R; Zwillich S; Chang C P; Callegari P E; Von Feldt J M; Fang Q; Weiner D B; Williams W V
CS Department of Medicine, University of Pennsylvania School of Medicine, Philadelphia 19104, USA.
SO Pathobiology : journal of immunopathology, molecular and cellular biology, (1995) Vol. 63, No. 2, pp. 100-8.
Journal code: 9007504. ISSN: 1015-2008.
CY Switzerland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199602
ED Entered STN: 12 Mar 1996
Last Updated on STN: 12 Mar 1996
Entered Medline: 23 Feb 1996
AB Synovial tissue is rarely available from patients with early synovitis, with the exception of synovial biopsies. However, T cell populations early in the development of synovitis may be enriched in antigen-specific cells and critical to disease pathogenesis. To investigate the T cell repertoire in early synovitis, we utilized a PCR protocol for detection of T cell receptor (TCR) transcripts present in small amounts of synovial tissue. To expand the substrate for PCR, preamplification of cDNA was performed with a 3' constant region primer plus either a mixture of variable region primers or random hexanucleotides. Utilizing this method improved the sensitivity of detection. This technique is applied here to the analysis of TCR transcripts in synovial biopsies from individuals with early rheumatoid arthritis (RA) and non-RA synovitis. TCR alpha-chain transcripts were detectable in 5/5 RA and 4/4 non-RA specimens evaluated, with beta-chain transcripts detected in 4/5 early RA and 4/4 non-RA specimens evaluated. Confirmation of transcripts by sequencing of cloned PCR products verified the specificity of amplification.
The most frequently expressed TCR V region families in early RA synovitis were V alpha 11, V alpha 14, V alpha 28, V beta 7, V beta 9 and V beta 17. Several of these V regions have previously been implicated in studies of chronic RA synovitis. J alpha and J beta region usage was similar to that seen in chronic RA, and conserved N region motifs were apparent. We conclude that it is possible to detect TCR transcripts in small synovial biopsies from individuals with early arthritis.(ABSTRACT TRUNCATED AT 250 WORDS)
AB . . . in antigen-specific cells and critical to disease pathogenesis. To investigate the T cell repertoire in early synovitis, we utilized a PCR protocol for detection of T cell receptor (TCR) transcripts present in small amounts of synovial tissue. To expand the substrate for PCR, preamplification of cDNA was performed with a 3' constant region primer plus either a mixture of variable region primers or random hexanucleotides. Utilizing

this method improved the sensitivity of detection. This technique is applied here to the analysis of TCR transcripts. . . with beta-chain transcripts detected in 4/5 early RA and 4/4 non-RA specimens evaluated. Confirmation of transcripts by sequencing of cloned PCR products verified the specificity of amplification. The most frequently expressed TCR V region families in early RA synovitis were V alpha 11, V alpha 14, V. . .

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